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APPLICATION NO	О.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.	
09/835,273	9/835,273 04/13/2001		James R. LaDine	12800-003001	4611	
44064	7590	09/30/2005		EXAM	EXAMINER	
THERMO) FINNIG	AN LLC	BORIN, MICHAEL L			
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SAN JOSI	SAN JOSE, CA 95134 ART UNIT PAPER N				PAPER NUMBER	
				1631		

DATE MAILED: 09/30/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

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	Application No.	Applicant(s)				
	09/835,273	LADINE ET AL.				
Office Action Summary	Examiner	Art Unit	·			
	Michael Borin	1631				
The MAILING DATE of this communication app Period for Reply	ears on the cover sheet w	ith the correspondence addres	ss			
A SHORTENED STATUTORY PERIOD FOR REPLY WHICHEVER IS LONGER, FROM THE MAILING DA - Extensions of time may be available under the provisions of 37 CFR 1.13 after SIX (6) MONTHS from the mailing date of this communication. - If NO period for reply is specified above, the maximum statutory period w - Failure to reply within the set or extended period for reply will, by statute, Any reply received by the Office later than three months after the mailing earned patent term adjustment. See 37 CFR 1.704(b).	ATE OF THIS COMMUNI 16(a). In no event, however, may a fill apply and will expire SIX (6) MOI cause the application to become A	CATION. reply be timely filed NTHS from the mailing date of this commu BANDONED (35 U.S.C. § 133).				
Status						
1) Responsive to communication(s) filed on 29 Ju	lv 2005.					
· _ · _ · _ · _ · · _ · · · · · _ ·	action is non-final.					
3) Since this application is in condition for allowant closed in accordance with the practice under E	•	• •	erits is			
Disposition of Claims						
4) Claim(s) <u>1,2,5-18 and 22-45</u> is/are pending in the	he application.					
4a) Of the above claim(s) is/are withdraw	vn from consideration.		•			
5) Claim(s) is/are allowed.		•				
6) Claim(s) <u>1,2,5-18 and 22-45</u> is/are rejected.						
7) Claim(s) is/are objected to.						
8) Claim(s) are subject to restriction and/or	election requirement.					
Application Papers						
9)☐ The specification is objected to by the Examiner	г.					
10)☐ The drawing(s) filed on is/are: a)☐ accepted or b)☐ objected to by the Examiner.						
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).						
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).						
11) The oath or declaration is objected to by the Ex	aminer. Note the attache	d Office Action or form PTO-1	152.			
Priority under 35 U.S.C. § 119						
12) Acknowledgment is made of a claim for foreign a) All b) Some * c) None of:	priority under 35 U.S.C.	§ 119(a)-(d) or (f).				
 Certified copies of the priority documents 	have been received.		,			
Certified copies of the priority documents	2. Certified copies of the priority documents have been received in Application No					
	3. Copies of the certified copies of the priority documents have been received in this National Stage					
application from the International Bureau						
* See the attached detailed Office action for a list of the certified copies not received.						
Attachment(s)						
1) X Notice of References Cited (PTO-892) 2) Notice of Draftsperson's Patent Drawing Review (PTO-948)		Summary (PTO-413) s)/Mail Date				
3) Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date		nformal Patent Application (PTO-152	2)			

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DETAILED ACTION

1. Claims 1,2,5-18, 22-45 are pending.

Amendment filed 07/29/2005 is acknowledged. The claims are amended to recite that each mass spectrometry system analyzes different protein sample. Consequently, the following new grounds of rejections are applied. Rejections not reiterated from previous Office actions are hereby withdrawn. The following rejections constitute the complete set presently being applied to the instant application.

Claim Rejections - 35 USC § 103.

2. Claims 1,2,5-18, 22-45 are rejected under 35 U.S.C. 103(a) as obvious over Zenhausern (US 20020094531; priority date 06/14/1999).

Zenhausern teaches a method for monitoring information in a medium, the medium comprising at least one biomolecule, the method comprising screening the medium with a screening means comprising a n number of sensing probes, where n is an integer of at least one so that more than one physical, chemical, or physico-chemical change. (claim 1). The n number of sensing probes is an array of mass-spectrometers (claims 3,9, paragraph [0047]). The biomolecules are, for example, proteins ([0027]). Monitoring a biomolecule includes interrogating the medium by coupling a sensor responsive to any changes of the medium and or biomolecule and its secondary products and includes direct detection and monitoring of biomolecular reactions in real-

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time (see Abstract and claims 1,13,14,). The results are subjected to multivariant

analysis (claims 20,21, paragraph 0012])

Zenhausern does not specifically teach preparing sample as instantly claimed,

namely submitting each of samples to a separation technique. However, such difference

would appear to be minor and prima facie obvious to one skilled in the art. It would be

obvious to one skilled in the art to use separation techniques to prepare protein samples

- see, for example Demirev et al reference (applied in the preceding Office actions)

which describe multiple separation of components. Further, see Zeng et al describing

preparation of samples for parallel HPLC/MS analysis of combinatorial libraries. In

addition, note that Zenhausern does teach that chromatography system (e.g., gas.

chromatography, liquid chromatography, or capillary electrophoresis) can be added in

conjunction with an appropriate sensor technique (e.g., mass spectrometer) - see

paragraph [0077].

With respect to claims 6,7, the reference is silent about the exact amount of

components, but it would within perview of skilled in the art to select the amount of

compounds of interest.

With respect to claims 12,17,18,36, selection of methods of preparing samples

and selecting appropriate time intervals of sampling would be obvious to an artisan as

a part of routine optimization.

With respect to claims 14-16,22,43,44, it would be obvious to an artisan that

measurement of a time course of changes in biological system can be made in

response to exposure of the biological system to a stimulus.

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Therefore it would be obvious to apply parallel mass spectrometry described in Zenhausern to any problem requiring multiple measurements of samples containing plurality of components, such as, for example, measurement of plurality of proteins from a quiescent or stimulated biological sample.

3. Claims 1,2,5-18, 22-45 are rejected under 35 U.S.C. 103(a) as obvious over Chang et al and Demirev et al (both references have been applied previously) and Chalmers et al. and Zeng et al in view of Zenhausern (US 20020094531), and further in view of Henry et al (Analytical Chemistry News &Features: Focus, April 1, 1999, p. 264A-268A), Cotter et al. (Journal of Mass spectrometry, 34, 1368-1372, 1999), and Orient et al. (Review of Scientific Instruments, March 1997, Volume 68, Issue 3, pp. 1393-1397).

There is well recognized need in the art to analyze complex multi-component protein mixtures with a combination of separation and analytical techniques, chromatography and mass spectrometry. Thus, Chang et al. discusses that in the GC-MS analysis there may be a complex sample which may consist of hundreds of components (col. 3, lines 27-31). Further, the reference teaches that in GC-MS experiment there may be a complex sample which may consist of hundreds of components (col. 4, lines 27-30), and that in a typical repetitive mass spectra acquisition

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operation, during an one-hour period of GC run, as many as 3600 might need to be acquired, processed and stored in a computer system (col. 2, last paragraph).

Demirev et al explore feasibility of a "massively parallel" mass spectrometry of proteins and suggests that practical implementations of parallel mass spectrometry seem feasible for protein libraries containing from several hundreds to several thousand individual components, or for monitoring the diversity of up to a thousand reaction products. See p. 2900, last two paragraphs. In their theoretical analysis, Demirev et al assume multiple separation of components but intentionally do not dwell into details of mass spectrometry arrangement (p. 2898, right column), but mention that there is a number of instrumental factors that must be accounted for in practical implementation of "parallel" mass spectrometric approach, such as e.g., detection efficiency and accuracy of mass spectrometry.

Chalmers et al. and Zeng et al, are other exemplary references describing chromatography/mass-spectrometry systems for analysis of complex peptide mixtures and proteome.

The primary references, although describing plurality of parallel separation units, do not teach multiple system of parallel mass-spectrometers that analyze the separated protein samples – in these references multiple samples are analyzed by the same mass-spectrometer, or a duet of mass-spectrometers analyzing various aspects of the same sample. This is understandable as an artisan would be aware of prohibitively high cost of mass-spectrometry system. However, the idea of combining of several analytical devices is well known in the art. For example, Zenhausern reference

addressed in the preceding rejection, teaches a multisensor array comprising a number of sensing probes, such as mass-spectrometers. Further, with regard to technical problems operating multiple mass-spectrometers (cost, size, weight), a new generation of simplified small and light-weight mass-spectrometers have been designed recently. see, for example, Henry et al., Cotter et al., and Orient et al.

Therefore, it would be *prima facie* obvious to analyze multiple protein samples using multiple mass-spectrometers instead of a single mass-spectrometers, because prior art teaches processing of multiple samples using an array of equivalent devices, such as mass spectrometers (Zenhausern), and also teaches availability of simplified mass spectrometers better suited for combining into such multiple analyzing arrays. One would expect that analyzing multiple samples using a set of analytical devices (i.e., mass spectrometers) would be at least as effective as using a single analytical device.

With regard to the dependent claims, if there are any differences from the prior art, these differences appear to be minor, as addressed in the preceding rejection.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Michael Borin whose telephone number is (571) 272-0713. The examiner can normally be reached on 9am-5pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ardin Marschel, Ph.D., can be reached on (571) 272-0718. The fax phone

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number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

> Michael Borin, Ph.D. **Primary Examiner** Art Unit 1631

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